

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/563,888A
Source: IFWO
Date Processed by STIC: 7/5/06

ENTERED



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/563,888A

DATE: 07/05/2006
TIME: 13:54:48

Input Set : A:\SEQLIST.TXT
Output Set: N:\CRF4\07052006\J563888A.raw

4 <110> APPLICANT: Chi-Hong B. Chen
5 Ralf Landgraf
7 <120> TITLE OF INVENTION: APTAMERS TO HUMAN EPIDERMAL GROWTH
8 FACTOR RECEPTOR-3
10 <130> FILE REFERENCE: 30448108USWO
12 <140> CURRENT APPLICATION NUMBER: 10/563,888A
13 <141> CURRENT FILING DATE: 2006-01-09
15 <150> PRIOR APPLICATION NUMBER: 60/488,679
16 <151> PRIOR FILING DATE: 2003-07-18
18 <150> PRIOR APPLICATION NUMBER: PCT/US04/23039
19 <151> PRIOR FILING DATE: 2004-07-16
21 <160> NUMBER OF SEQ ID NOS: 20
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 4026
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
31 atgagggcga acgacgtct gcaggtgctg ggcttgcttt tcagcctggc ccggggctcc 60
32 gaggtgggca actctcaggc agtgtgtcct gggactctga atggcctgag tgtgaccggc 120
33 gatgctgaga accaatacca gacactgtac aagctctacg agaggtgtga ggtggtgatg 180
34 gggAACCTTG agattgtgct cacgggacac aatgccgacc ttccttctt gcagtggatt 240
35 cgagaagtga caggctatgt ctcgtggcc atgaatgaat tctctactt accattgccc 300
36 aacctcccgcg tggtgcgagg gaccagggtc tacgatggga agtttgcatt ctctgtcatg 360
37 ttgaactata acaccaactc cagccacgct ctgcgccagc tccgcttgcac tcagctcacc 420
38 gagattctgt caggggggtgt ttatatttag aagaacgata agctttgtca catggacaca 480
39 attgacttggaa gggacatcgt gaggggaccga gatgctgaga tagtggtgaa ggacaatggc 540
40 agaagctgtc cccccctgtca tgagggttgc aaggggcgt gctggggtcc tggatcagaa 600
41 gactgccaga cattgaccaa gaccatctgt gtcctcagt gtaatggtca ctgtttggg 660
42 cccaaacccca accagtgtcg ccatgatgag tgtgcgggg gctgtcagg ccctcaggac 720
43 acagactgtcttgcg gcacttcaat gacagtggag cctgtgtacc tcgctgtcca 780
44 caggcttgg tctacaacaa gctaactttc cagctggAAC ccaatccccca caccatgtat 840
45 cagtatggag gagtttgtgt agccagctgt cccccataact ttgtggtgaa tcaaaatcc 900
46 tgtgtcaggc cctgtctcc tgacaagatg gaagtagata aaaatgggt caagatgtgt 960
47 gaggcttgg gggactatg tcccaaagcc tgtgaggaa caggctctgg gagccgcttc 1020
48 cagactgtgg actcgagcaa cattgatgga tttgtgaact gcaccaagat cctggcaac 1080
49 ctggactttc tgatcaccgg cctcaatggc gaccctggc acaagatccc tgccctggac 1140
50 ccagagaagc tcaatgtctt cggacagta cgggagatca caggttacct gaacatccag 1200
51 tcctggccgc cccacatgca caacttcagt gtttttcca atttgacaac cattggaggc 1260
52 agaaggctct acaacccggg cttctcattt ttgatcatga agaacttggaa tgtcacatct 1320
53 ctgggcttcc gatccctgaa gggaaatttagt gctggcgtt tctatataag tgccaaatagg 1380
54 cagctctgtc accaccactc ttgaaactgg accaagggtgc ttccggggcc tacgaaagag 1440
55 cgactagaca tcaagcataa tcggccgccc agagactgctg tggcagaggg caaagtgtgt 1500

R,
b

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107	1	5	10	15
108	Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr			
109	20	25	30	
110	Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr			
111	35	40	45	
112	Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu			
113	50	55	60	
114	Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile			
115	65	70	75	80
116	Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr			
117	85	90	95	
118	Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp			
119	100	105	110	
120	Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser			
121	115	120	125	
122	His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser			
123	130	135	140	
124	Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr			
125	145	150	155	160
126	Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val			
127	165	170	175	
128	Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly			
129	180	185	190	
130	Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr			
131	195	200	205	
132	Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn			
133	210	215	220	
134	Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp			
135	225	230	235	240
136	Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val			
137	245	250	255	
138	Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu			
139	260	265	270	
140	Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala			
141	275	280	285	
142	Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala			
143	290	295	300	
144	Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys			
145	305	310	315	320
146	Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser			
147	325	330	335	
148	Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val			
149	340	345	350	
150	Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu			
151	355	360	365	
152	Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu			
153	370	375	380	
154	Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln			
155	385	390	395	400

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156 Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
 157 405 410 415
 158 Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
 159 420 425 430
 160 Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
 161 435 440 445
 162 Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
 163 450 455 460
 164 His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
 165 465 470 475 480
 166 Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
 167 485 490 495
 168 Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
 169 500 505 510
 170 Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
 171 515 520 525
 172 Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
 173 530 535 540
 174 His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Gly
 175 545 550 555 560
 176 Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
 177 565 570 575
 178 Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
 179 580 585 590
 180 Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
 181 595 600 605
 182 Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
 183 610 615 620
 184 Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
 185 625 630 635 640
 186 His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
 187 645 650 655
 188 Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
 189 660 665 670
 190 Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu
 191 675 680 685
 192 Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe
 193 690 695 700
 194 Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe
 195 705 710 715 720
 196 Gly Thr Val His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys
 197 725 730 735
 198 Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser
 199 740 745 750
 200 Phe Gln Ala Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His
 201 755 760 765
 202 Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln
 203 770 775 780
 204 Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg

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205	785	790	795	800
206	Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val			
207	805	810	815	
208	Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His			
209	820	825	830	
210	Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val			
211	835	840	845	
212	Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys			
213	850	855	860	
214	Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu			
215	865	870	875	880
216	Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser			
217	885	890	895	
218	Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr			
219	900	905	910	
220	Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu			
221	915	920	925	
222	Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met			
223	930	935	940	
224	Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu			
225	945	950	955	960
226	Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu			
227	965	970	975	
228	Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro			
229	980	985	990	
230	His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu			
231	995	1000	1005	
232	Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala Thr			
233	1010	1015	1020	
234	Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu Asn Arg			
235	1025	1030	1035	1040
236	Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro			
237	1045	1050	1055	
238	Met Asn Gln Gly Asn Leu Gly Gly Ser Cys Gln Glu Ser Ala Val Ser			
239	1060	1065	1070	
240	Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser Leu His Pro Met Pro			
241	1075	1080	1085	
242	Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu Gly His Val Thr Gly Ser			
243	1090	1095	1100	
244	Glu Ala Glu Leu Gln Glu Lys Val Ser Met Cys Arg Ser Arg Ser Arg			
245	1105	1110	1115	1120
246	Ser Arg Ser Pro Arg Pro Arg Gly Asp Ser Ala Tyr His Ser Gln Arg			
247	1125	1130	1135	
248	His Ser Leu Leu Thr Pro Val Thr Pro Leu Ser Pro Pro Gly Leu Glu			
249	1140	1145	1150	
250	Glu Glu Asp Val Asn Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly			
251	1155	1160	1165	
252	Thr Pro Ser Ser Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser			
253	1170	1175	1180	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; N Pos. 35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54
Seq#:14; N Pos. 55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74
Seq#:14; N Pos. 75,76,77,78,79,80,81,82,83

VERIFICATION SUMMARY

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L:727 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:731 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:732 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14